



A DOCPHOENIX

SEQUENCE LISTING

- (1) INFORMATION FOR SEQ ID NO: 1
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 305base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 (ii) MOLECULE TYPE: cDNA
 (iii) SEQUENCE DESCRIPTION: SEQ ID NO: 1

Seq ID No. 1# Sequence of 31.2 clone:

5'- ATCGCCGTAA TTGCCATGTT TTCCCTCTCA CCGGAATCCT ACGTTATCC
 CCTTACCTTC GTGAACATTA CAGTAGGAAT CGGTGGTCCA ATTATCAACT
 TAATTTTGGG CGCATCTGTT CGTGTTAACT AGAAGCCATG TATACATACA
 ATACAACATG GTTCACTCCT CCTACAGATT ATGAGTTGAA CTTTATAAT
 AAGTTGTAAT AATGGCTTCT GAATAAGGAG AAGAGGAGCC TCTGTTTGT
 TTAATTATTA CAGATGTGAT ATCGTTCAAC AACTTTGATT CTGCGAAAA
 AAAAA-3'

- (2) INFORMATION FOR SEQ ID NO:2
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 297 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 (ii) MOLECULE TYPE: cDNA
 (iii) SEQUENCE DESCRIPTION: SEQ ID NO: 2

Seq ID No.2# Sequence of 21.2 Clone:

5'- AGAAGTACCT GAAAGGAAGC TTAACGAGGT GAACATCCAT
 TGCAGCCAGC CCTGGAATCT GTACAGGGCA ACTCTGAACC GGAATTATTT
 TAATAACCCG TGGGCAATGA TTGCAATTAT GGCTCGTTTG GTATTACTTC
 TACTCACTTA GACACAACTG TATTTACGGT TTTCGCTGGA ATTGTAATTG
 TTGGAGCGAC AAAATAGATG GTCACAACTT ATTGGTGAGA GTATCAGTGT
 GCTCTTCTTT ATCGTCTTTA ACTCTCCGTG GTAATTACTT TGACAATATT
 CATACAT -3'

Does Not Comply
 Corrected Diskette Needed

Invalid sequence listing
 format. See below for
 correct format.

SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 (i) APPLICANT:
 (ii) TITLE OF INVENTION:
 (iii) NUMBER OF SEQUENCES:
 (iv) CORRESPONDENCE ADDRESS:
 (A) ADDRESSEE:
 (B) STREET:
 (C) CITY:
 (D) STATE:
 (E) COUNTRY:
 (F) ZIP:
 (v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE:
 (B) COMPUTER:
 (C) OPERATING SYSTEM:
 (D) SOFTWARE:
 (vi) CURRENT APPLICATION DATA:
 (A) APPLICATION NUMBER:
 (B) FILING DATE:
 (C) CLASSIFICATION:
 (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER:
 (B) FILING DATE:
 (viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME:
 (B) REGISTRATION NUMBER:
 (C) REFERENCE/DOCKET NUMBER:
 (ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE:
 (B) TELEFAX:
 (C) TELEX:
 (2) INFORMATION FOR SEQ ID NO: X:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH:
 (B) TYPE:
 (C) STRANDEDNESS:
 (D) TOPOLOGY:
 (ii) SEQUENCE DESCRIPTION: SEQ ID NO: X:

* Please note: Only
 applications prior to July 1,
 1998 may use the old
 sequence rules format, unless
 there is a related application
 filed prior to July 1, 1998.

* New sequence rules listing
 example and feature explanation
 has been attached also.

*New sequence rules
for cases filed
after July 1, 1998
with no prior
related applications.*

APPENDIX 3
SPECIMEN SEQUENCE LISTING

<110> Smith, John; Smithgene Inc.

<120> Example of a Sequence Listing

<130> 01-00001

<140> PCT/EP98/00001
<141> 1998-12-31

<150> US 08/999,999
<151> 1997-10-15

<160> 4

<170> PatentIn version 2.0

<210> 1
<211> 389
<212> DNA
<213> Paramecium sp.

<220>
<221> CDS
<222> (279)...(389)

<300>
<301> Doe, Richard
<302> Isolation and Characterization of a Gene Encoding a
Protease from Paramecium sp.
<303> Journal of Genes
<304> 1
<305> 4
<306> 1-7
<307> 1988-06-31
<308> 123456
<309> 1988-06-31

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tgatgtggca	attgctggca	gtgccacagg	cttttcagcc	aggcttaggg	tgggttccgc		180
cgcgggcgcg	cggccctct	cgcgtctct	tcgcgcctct	ctctcgctct	cctctcgctc		240

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ggacctgatt	aggtgagcag	gaggaggggg	cagtttagc	atg Met 1	gtt Val	tca Ser	atg Met	ttc Phe 5	agc Ser	296						
ttg Leu	tct Ser	ttc Phe	aaa Lys 10	tgg Trp	cct Pro	gga Gly	ttt Phe	tgt Cys 15	ttg Leu	ttt Phe	ggt Val	tgt Cys	ttg Leu 20	ttc Phe	caa Gln	344
tgt Cys	ccc Pro	aaa Lys 25	gtc Val	ctc Leu	ccc Pro	tgt Cys	cac His 30	tca Ser	tca Ser	ctg Leu	cag Gln	ccg Pro 35	aat Asn	ctt Leu	389	
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<211>	37															
<212>	PRT															
<213>	Paramecium sp.															
<400>	2															
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Phe	Val	Cys	Leu 20	Phe	Gln	Cys	Pro	Lys 25	Val	Leu	Pro	Cys	His 30	Ser	Ser	
Leu	Gln	Pro 35	Asn	Leu												
<210>	3															
<211>	11															
<212>	PRT															
<213>	Artificial Sequence															
<220>																
<223>	Designed peptide based on size and polarity to act as a linker between the alpha and beta chains of Protein XYZ.															
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<400>	4															
000																

[Annex VIII follows]

Numeric Identifier	Definition	Comments and format	Mandatory (M) or optional (O).
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials.	M.
<120>	Title of Invention		M.
<130>	File Reference	Personal file reference	M when filed prior to assignment of appl. number.
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available.
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available.
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120.
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable.
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M.
<170>	Software	Name of software used to create the Sequence Listing.	O.
<210>	SEQ ID NO:1:	Response shall be an integer representing the SEQ ID NO shown.	M.
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues.	M.

Numeric Identifier	Definition	Comments and format	Mandatory (M) or optional (O).
<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M.
<213>	Organism	Scientific name, i.e. Genus/ species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M.
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence.
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/ amino acids in feature.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence.
<223>	Other Information	Other relevant information; four lines maximum	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	O.
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials.	O.
<302>	Title		O.
<303>	Journal		O.
<304>	Volume		O.
<305>	Issue		O.
<306>	Pages		O.
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy.	O.
<308>	Database Accession Number	Accession number assigned by database including database name.	O.
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy.	O.
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999.	O.
<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd.	O.
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd.	O.
<313>	Relevant Residues	FROM (position) TO (position)	O.
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence.	M.